AMENDMENTS TO THE CLAIMS:

Please amend claims 1-27 as follows:

1. (Original): A method for controlling the expression of heterologous genes in microorganisms associated with cells of higher organisms consisting of:

a. a regulatory system that can be controlled by a chemical effector;

b. a host microorganism that contains the regulatory system capable of interacting with or associating with cells of higher organisms;

c. an effector chemical compound that is a salicylate or salicylate derivative that can be transported through the associated higher organism and activate or repress the expression of the modified host microorganism.

2. (Original): The method claimed in claim 1, wherein at least one of the regulatory proteins is controlled by salicylate, anthranylate, 2-acetyl salicylate, 4-chloro-salicylate, 5-chloro-salicylate, 3,5-dichloro-salicylate, 5-methoxy-salicylate, benzoate, 3-methyl-benzoate, 2-methoxy-benzoate, 3-methyl-salicylate, 4-methyl-salicylate, 5-methyl-salicylate, any other salicylate derivative that conserves the carboxylic C-1 group in the aromatic ring, or mixture of the same.

3. (Original): The method claimed in claim 2, wherein the regulatory system consists of at least one regulatory protein that belongs to the LysR/NahR family of regulators.

4. (Original): The method as claimed in claim 2, wherein the regulatory system consists of at least one derivative of the XylS/AraC family of regulators.

5. (Original): The method as claimed in claim 2, wherein the regulatory system consists of a regulatory protein belonging to the MarR family of regulators.

6. (Original): The method as claimed in claim 2, wherein the regulatory system consists of a system of nahR/Psal expression, or mutants of the same elements.

7. (Original): The method as claimed in claim 2, wherein the regulatory system consists of a system of xylS/Pm expression, or mutants of the same elements, capable of responding to any of the chemical compounds cited in claim 2.

8. (Original): The method as claimed in claim 2, wherein the regulatory system consists of a genetic cascade circuit that consists of:

a. the transcriptional regulator NahR, or a mutant form of the same, and the transcriptional regulator XylS, or a mutant form of the same, wherein the transcriptional regulators are placed in hierarchical order in such a way that the transcriptional regulator NahR, or a mutant form of the same, stimulates the expression of transcriptional regulator XylS, or a mutant form of the same, and wherein the transcriptional regulator NahR, or a mutant form of the same, and the transcriptional regulator XylS or a mutant form of the same, respond to the same inducer;
b. a terminal target promoter, wherein said terminal target promoter is characterized by its dose-dependent sensitivity to the transcriptional regulator XylS, or a mutant form of the same.

9. (Original): A method as claimed in claim 1 wherein the cell capable of associating with higher organisms and containing the system regulating heterologous gene expression is a prokaryotic cell.

10. (Original): A method as claimed in claim 9 wherein the prokaryotic cell is a gram-negative bacteria.

11. (Original): A method as claimed in claim 10 wherein because the gram-negative bacterial cell is a bacteria of the genus Salmonella.

12. (Currently Amended): A method as claimed in ~~any of the above~~ claim[[s]] 9 ~~to 11~~ that has been developed to control the expression of therapeutic proteins or a diagnostic protein in an attenuated bacteria associated with cells of higher organisms.

13. (Original): A method as claimed in claim 12 wherein the expression of a heterologous antigen in an attenuated bacteria associated with cells of higher organisms is controlled for use as a recombinant live vaccine.

14. (Original): A method as claimed in claim 12 wherein the expression of at least one antitumoral protein that has a certain tropism for tumoral cells in a higher organism is controlled in an attenuated bacteria associated with cells of said higher organism.

15. (Original): The method as claimed in claim 14 wherein the antitumoral protein is selected from a group consisting of an interleukin, cytokine, toxin, cytotoxic protein, or antiangiogenic protein.

16. (Original): The method as claimed in claim 9 wherein the bacteria also contains a regulatory system sensitive to salicylate or its derivatives and a target promoter, which controls the expression of a suicide gene that encodes a product toxic to the host cell.

17. (Original): The method is used as claimed in claim 9 to study the genes implicated in pathogenesis using bacteria with conditional phenotypes.

18. (Original): The method is used as claimed in claim 16 for the selective elimination of microorganisms in bioreactors.

19. (Original): The method is used as claimed in claim 16 for the selective elimination of cells that can be selectively infected with a bacteria or virus that produces a toxic process or a biomolecule capable of triggering apoptosis or any other mechanism of cell death in malignant cells.

20. (Original): The method used to control the expression of heterologous therapeutic proteins or heterologous diagnostic proteins in microorganisms associated with cells of higher organisms consists of:

a. a bacterial cell that contains a regulatory system that can be controlled by salicylate or salicylate derivative as a chemical effector, which is associated specifically to cells of a higher organism;
b. the induction of the expression of said heterologous therapeutic proteins or heterologous diagnostic proteins by administering salicylate or salicylate derivatives to the higher organism hosting the modified cell.

21. (Original): The method as claimed in claim 20 wherein the regulatory system is selected from among the group formed by at least one regulatory protein that belongs to the LysR/NahR family of regulators, at least one derivative of the XylS/AraC family of regulators, at least one regulatory protein that belongs to the family of MarR regulators, at least one nahR/Psal regulatory system, or mutant of the same elements, at least one system of xylS/Pm expression, or mutant of the same elements, a genetic cascade circuit that consists of the transcriptional regulator NahR, or a mutant form of the same, and the transcriptional regulator XylS, or a mutant form of the same, or a combination of the above.

22. (Currently Amended): A method as claimed in ~~any of the above~~ claim[[s]] 20 ~~to 21~~ wherein said heterologous therapeutic protein is a heterologous antigen, an antitumoral protein, or mixture of the same.

23. (Original): The regulatory system of heterologous gene expression in bacteria is associated with tumoral cells of a higher organism and controlled by salicylate or salicylate derivatives to regulate the expression of at least one antitumoral protein.

24. (Original): A use as claimed in claim 23 wherein the antitumoral protein expressed is selected from the group consisting of an interleukin, cytokine, toxin, cytotoxic protein, or antiangiogenic protein.

25. (Original): The use of a system regulating heterologous gene expression in bacteria associated with cells of a higher organism that is controlled by salicylate or salicylate derivatives to regulate the expression of a heterologous antigen for use as a recombinant live vaccine.

26. (Currently Amended): The use of a regulatory system of heterologous gene expression in bacteria associated with cells of a higher organism, as claimed in ~~any of~~ claim[[s]] 23 ~~to 25~~, wherein said regulatory system is selected from a group consisting of at least one regulatory protein pertaining to the LysR/NahR family of regulators, at least one derivative of the XylS/AraC family of regulators, at least one regulatory protein pertaining to the MarR family of regulators, at least one nahR/Psal regulatory system, or mutants of the same elements, at least one xylS/Pm regulatory system, or mutants of the same elements, a genetic cascade circuit that consists of the transcriptional regulator NahR, or a mutant form of the same, and the transcriptional regulator XylS, or a mutant form of the same, or a combination of the above.

27. (Original): The modified bacteria that contains the regulatory system used is selected from the group consisting of at least one regulatory protein belonging to the LysR/NahR family of regulators, at least one derivative of the XylS7AraC family of regulators, at least one regulatory protein belonging to the MarR family of regulators, at least one nahR/Psal regulatory system, or mutants of the same elements, at least one system of xylS/Pm expression, or mutants of the same elements, a genetic circuit cascade that consists of the transcriptional regulator NahR, or a mutant form of the same, and the transcriptional regulator XylS, or a mutant form of the same, or a combination of the above, in the method of control of heterologous gene expression in microorganisms associated to cells of higher organisms. as claimed in claim 1.